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☐ 1: Wei Sheng Wu Xue Bao 1993  
Aug;33(4):280-4

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## [The isolation and identification of a *Clostridium botulinum* serotype A strain]

[Article in Chinese]

Liu S, Wu T, Yang Z, Yuan T.

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Institute of Biotechnology, Sichuan University, Chengdu

319 soil specimens were collected from different places in China for isolating *Clostridium botulinum*. A strain of *Clostridium botulinum* was isolated from a culture of soil specimens in Ruogai of Sichuan Province, the strain was called As-3. The As-3 was identified as *Clostridium botulinum* serotype A according to its biological properties, biochemical, serological and toxicological characteristics, DNA determination. Its DNA G + C mol is 24.9%. The toxin produced by As-3 strain can only be neutralized by type A antiserum.

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PMID: 8256440 [PubMed - indexed for MEDLINE]

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# SWISS-PROT: BXA1\_CLOBO

The section of the sequence BXA1\_CLOBO (P10845) you have selected corresponds to:

CONFLICT 479 479 E -> P (IN REF. 9).

In one-letter code:

1	11	21	31	41	51	
1 PFVVKQFNKY	DPVNGVDIAY	IKIPNVGQMQ	PVKAFKIHNK	IWVIPERDTF	TNPEEGDLNP	60
61 PPEAKQVPVS	YYDSTYLSTD	NEKDNYLKGV	TKLFERIYST	DLGRMLLTSI	VRGIPFWGGS	120
121 TIDTELKVID	TNCINVIQPD	GSYRSEELNL	VIIGPSADII	QFECKSFGHE	VLNLTRNGYG	180
181 STQYIRFSPD	FTFGFEESLE	VDTNPLLGA	KFATDPAVTL	AHELIHAGHR	LYGIAINPNR	240
241 VFKVNTNAYY	EMSGLEVSFE	ELRTFGGHDA	KFIDSLQENE	FRLYYYNKFK	DIASLTNKAK	300
301 SIVGTTASLQ	YMKNVFKEY	LLSEDTSGKF	SVDKLFKFDKL	YKMLTEIYTE	DNFVKFFKVL	360
361 NRKTYLNFDK	AVFKINIVPK	VNYTIYDGFN	LRNTNLAANF	NGQNTNINNM	NFTKLKNFTG	420
421 LFEFYKLLCV	RGIITSKTKS	LDKGYNKALN	DLCIKVNNWD	LFFSPSEDNF	TNDLNKGEEI	480
481 TSDTNIEAAE	ENISLDLIQQ	YYLTFNFDNE	PENISIENLS	SDIIGQLELM	PNIERFPNGK	540
541 KYELDKYTMF	HYLRAQEFEH	GKSRIALTNS	VNEALLNPSR	VYTFSSSDYV	KKVKNKATEAA	600
601 MFLGWVEQLV	YDFTDETSEV	STTDKIADIT	IIPIYIGPAL	NIGNMLYKDD	FVGALIFSGA	660
661 VILLEFIPEI	AIPVLGTFAL	VSYIANKVLT	VQTIDNALS	RNEKWDEVYK	YIVTNWLAKV	720
721 NTQIDLIRKK	MKEALENQAE	ATKAIINYQY	NQYTEEEKNN	INFNIDDLSS	KLNESINKAM	780
781 ININKFLNQC	VSYLMNSMI	PYGVKRLEDF	DASLKDALLK	YIYDNRGTLI	GQVDRKDKV	840
841 NNTLSTDIPF	QLSKYVDNQR	LLSTFTEYIK	NIINTSILNL	RYESNHLIDL	SRYASKINIG	900
901 SKVNFDPIDK	NQIQLFNLES	SKIEVILKNA	IVYNSMYENF	STSFWIRIPK	YFNSISLNNE	960
961 YTIINCMENN	SGWKVSLNYG	EIIWTLQDTQ	EIKQRVVFYK	SQMINISDYI	NRWIFVTITN	1020
1021 NRLNNSKIYI	NGRLIDQKPI	SNLGNIHASN	NIMFKLDGCR	DTHRYIWIKY	FNLFDKELNE	1080
1081 KEIKDLYDNQ	SNSGILKDFW	GDYLYQDKPY	YMLNLYDPNK	YVDVNNVGIR	GYMYLKGPGRG	1140
1141 SVMTTNIYLN	SSLYRGTKFI	IKKYASGNKD	NIVRNNDRVY	INVVVKNKEY	RLATNASQAG	1200
1201 VEKILSALEI	PDVGNLSQVV	VMKSKNDQGI	TNKCKMNLQD	NNGNDIGFIG	FHQFNNIACL	1260
1261 VASNWYNRQI	ERSSRTLGC	WEFIPVDDGW	GERPL			

In three-letter code:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1 Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly	15
16 Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Val	Gly	Gln	Met	Gln	30
31 Pro	Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	45
46 Glu	Arg	Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	60
61 Pro	Pro	Glu	Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	75
76 Tyr	Leu	Ser	Thr	Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	90
91 Thr	Lys	Leu	Phe	Glu	Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	105
106 Leu	Leu	Thr	Ser	Ile	Val	Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	120
121 Thr	Ile	Asp	Thr	Glu	Leu	Lys	Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	135
136 Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr	Arg	Ser	Glu	Glu	Leu	Asn	Leu	150
151 Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Phe	Glu	Cys	Lys	165
166 Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr	Arg	Asn	Gly	Tyr	Gly	180
181 Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe	Thr	Phe	Gly	Phe	195
196 Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu	Gly	Ala	Gly	210

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211 Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu Leu Ile 225
226 His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn Arg 240
241 Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu 255
256 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala 270
271 Lys Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr 285
286 Tyr Asn Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys 300
301 Ser Ile Val Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val 315
316 Phe Lys Glu Lys Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe 330
331 Ser Val Asp Lys Leu Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr 345
346 Glu Ile Tyr Thr Glu Asp Asn Phe Val Lys Phe Phe Lys Val Leu 360
361 Asn Arg Lys Thr Tyr Leu Asn Phe Asp Lys Ala Val Phe Lys Ile 375
376 Asn Ile Val Pro Lys Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn 390
391 Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr 405
406 Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly 420
421 Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr 435
436 Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys Ala Leu Asn 450
451 Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro 465
466 Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile 480
481 Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu 495
496 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu 510
511 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly 525
526 Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys 540
541 Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala 555
556 Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser 570
571 Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe 585
586 Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala 600
601 Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp 615
616 Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr 630
631 Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met 645
646 Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala 660
661 Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu 675
676 Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr 690
691 Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp 705
706 Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val 720
721 Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu 735
736 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr 750
751 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile 765
766 Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met 780
781 Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu 795
796 Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe 810
811 Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn 825
826 Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val 840
841 Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr 855
856 Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys 870
871 Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn 885
886 His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly 900
901 Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu 915
916 Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala 930
931 Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp 945
946 Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu 960
961 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val 975
976 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln 990
991 Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn 1005
1006 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn 1020
1021 Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile 1035
1036 Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn 1050
1051 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr 1065
1066 Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu 1080
1081 Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile 1095
1096 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr 1110

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1111 Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn 1125  
1126 Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly 1140  
1141 Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg 1155  
1156 Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp 1170  
1171 Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val 1185  
1186 Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly 1200  
1201 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn 1215  
1216 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile 1230  
1231 Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp 1245  
1246 Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu 1260  
1261 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg 1275  
1276 Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp 1290  
1291 Gly Glu Arg Pro Leu

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# SWISS-PROT: BXA1\_CLOBO

The section of the sequence BXA1\_CLOBO (P10845) you have selected corresponds to:

CONFLICT 875 875 T -> L (IN REF. 8).

In one-letter code:

1	11	21	31	41	51	
1	PFVVKQFNKY	DPVNGVDIAY	IKIPNVGQMQ	PVKAFKIHNK	IWVIPERDTF	TNPEEGDLNP 60
61	PPEAKQVPVS	YYDSTYLLSTD	NEKDNYLKGV	TKLFERIYST	DLGRMLLTSI	VRGIPFWGGS 120
121	TIDTELKVID	TNCINVIQPD	GSYRSEELNL	VIIGPSADII	QFECKSFGHE	VLNLTRNGYG 180
181	STQYIRFSPD	FTFGFEESLE	VDTNPLLGA	KFATDPAVTL	AHELIHAGHR	LYGIAINPNR 240
241	VFKVNTNAYY	EMSGLEVSFE	ELRTFGGHDA	KFIDSLQENE	FRLYYYNKFK	DIASLTNKA 300
301	SIVGTTASLQ	YMKNVFKEY	LLSEDTSGKF	SVDKLKFDKL	YKMLTEIYTE	DNFVKFFKVL 360
361	NRKTYLNFDK	AVFKINIVPK	VNYTIYDGFN	LRNTNLAANF	NGQNTNINNM	NFTKLKNFTG 420
421	LFEFYKLLCV	RGIITSKTKS	LDKGYNKALN	DLCIKVNNWD	LFFSPSEDNF	TNDLNKGEEI 480
481	TSDTNIEAAE	ENISLDLIQQ	YYLTFNFDNE	PENISIENLS	SDIIGQLELM	PNIERFPNGK 540
541	KYELDKYTMF	HYLRAQEFEH	GKSRIALTNS	VNEALLNPSR	VYTFSSDYV	KKVKNKATEAA 600
601	MFLGWVEQLV	YDFTDETSEV	STTDKIADIT	IIIPYIGPAL	NIGNMLYKDD	FVGALIFSGA 660
661	VILLEFIPEI	AIPVLGTFAL	VSYIANKVLT	VQTIDNALSK	RNEKWDEVYK	YIVTNWLAKV 720
721	NTQIDLIRKK	MKEALENQAE	ATKAIINYQY	NQYTEEEKNN	INFNIDDLSS	KLNESINKAM 780
781	ININKFLNQC	SVSYLMNSMI	PYGVRLEDF	DASLKDALLK	YIYDNRGTLI	GQVDRDKDKV 840
841	NNTLSTDIPF	QLSKYVDNQR	LLSTFTEYIK	NIINTSILNL	RYESNHLIDL	SRYASKINIG 900
901	SKVNFDPIDK	NQIQLFNLES	SKIEVILKNA	IVYNSMYENF	STSEWIRIPK	YFNSISLNNE 960
961	YTIINCMENN	SGWKVSLNYG	EIIWTLQDTQ	EIKQRVVFYK	SQMINISDYI	NRWIFVTITN 1020
1021	NRLNNSKIYI	NGRLIDQKPI	SNLGNIHASN	NIMFKLDGCR	DTHRYIWIKY	FNLFDKELNE 1080
1081	KEIKDLYDNQ	SNSGILKDFW	GDYLYQDKPY	YMLNLYDPNK	YVDVNNVGIR	GYMYLKGPGRG 1140
1141	SVMTTNIYLN	SSLYRGTKFI	IKKYASGNKD	NIVRNNDRVY	INVVVKNKEY	RLATNASQAG 1200
1201	VEKILSALEI	PDVGNSQVQV	VMKSKNDQGI	TNKCKMNLQD	NNGNDIGFIG	FHQFNNIKAL 1260
1261	VASNWYNRQI	ERSSRTLGC	WEFIPVDDGW	GERPL		

In three-letter code:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly	15
16	Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Val	Gly	Gln	Met	Gln	30
31	Pro	Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	45
46	Glu	Arg	Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	60
61	Pro	Pro	Glu	Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	75
76	Tyr	Leu	Ser	Thr	Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	90
91	Thr	Lys	Leu	Phe	Glu	Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	105
106	Leu	Leu	Thr	Ser	Ile	Val	Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	120
121	Thr	Ile	Asp	Thr	Glu	Leu	Lys	Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	135
136	Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr	Arg	Ser	Glu	Glu	Leu	Asn	Leu	150
151	Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Phe	Glu	Cys	Lys	165
166	Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr	Arg	Asn	Gly	Tyr	Gly	180
181	Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe	Thr	Phe	Gly	Phe	195
196	Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu	Gly	Ala	Gly	210

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211 Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu Leu Ile 225
226 His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn Arg 240
241 Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu 255
256 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala 270
271 Lys Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr 285
286 Tyr Asn Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys 300
301 Ser Ile Val Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val 315
316 Phe Lys Glu Lys Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe 330
331 Ser Val Asp Lys Leu Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr 345
346 Glu Ile Tyr Thr Glu Asp Asn Phe Val Lys Phe Phe Lys Val Leu 360
361 Asn Arg Lys Thr Tyr Leu Asn Phe Asp Lys Ala Val Phe Lys Ile 375
376 Asn Ile Val Pro Lys Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn 390
391 Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr 405
406 Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly 420
421 Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr 435
436 Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys Ala Leu Asn 450
451 Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro 465
466 Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile 480
481 Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu 495
496 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu 510
511 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly 525
526 Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys 540
541 Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala 555
556 Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser 570
571 Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe 585
586 Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala 600
601 Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp 615
616 Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr 630
631 Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met 645
646 Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala 660
661 Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu 675
676 Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr 690
691 Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp 705
706 Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val 720
721 Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu 735
736 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr 750
751 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile 765
766 Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met 780
781 Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu 795
796 Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe 810
811 Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn 825
826 Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val 840
841 Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr 855
856 Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys 870
871 Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn 885
886 His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly 900
901 Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu 915
916 Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala 930
931 Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp 945
946 Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu 960
961 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val 975
976 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln 990
991 Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn 1005
1006 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn 1020
1021 Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile 1035
1036 Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn 1050
1051 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr 1065
1066 Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu 1080
1081 Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile 1095
1096 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr 1110

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1111 Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn 1125  
1126 Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly 1140  
1141 Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg 1155  
1156 Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp 1170  
1171 Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val 1185  
1186 Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly 1200  
1201 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn 1215  
1216 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile 1230  
1231 Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp 1245  
1246 Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu 1260  
1261 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg 1275  
1276 Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp 1290  
1291 Gly Glu Arg Pro Leu

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# SWISS-PROT: BXA1\_CLOBO

The section of the sequence [BXA1\\_CLOBO](#) (P10845) you have selected corresponds to:

CONFLICT 891 891 S -> K (IN REF. 8).

In one-letter code:

1	11	21	31	41	51	
1	PFVVKQFNKY	DPVNGVDIAY	IKIPNVGQMQ	PVKAFKIHNK	IWVIPERDTF	TNPEEGDLNP 60
61	PPEAKQVPVS	YYDSTYLSTD	NEKDNYLKGV	TKLFERIYST	DLGRMLLTSI	VRGIPFWGGS 120
121	TIDTELKVID	TNCINVIQPD	GSYRSEELNL	VIIGPSADII	QFECKSFGHE	VLNLTRNGYG 180
181	STQYIRFSPD	FTFGFEESLE	VDTNPLLGA	KEATDPAVTL	AHELIHAGHR	LYGIAINPNR 240
241	VFKVNTNAYY	EMSGLEVSFE	ELRTFGGHDA	KFIDSLQENE	FRLYYYNKFK	DIASLTNKAK 300
301	SIVGTTASLQ	YMKNVFKEY	LLSEDTSGKF	SVDKLFKFDKL	YKMLTEIYTE	DNFVKFFKVL 360
361	NRKTYLNFDK	AVFKINIVPK	VNYTIYDGFN	LRNTNLAANF	NGQNTNINNM	NFTKLKNFTG 420
421	LFEFYKLLCV	RGITTSKTKS	LDKGYNKALN	DLCIKVNNWD	LFFSPSEDNF	TNDLNKGEEI 480
481	TSDTNIEAAE	ENISLDLIQQ	YYLTFNFDNE	PENISIENLS	SDIIGQLELM	PNIERFPNGK 540
541	KYELDKYTMF	HYLRAQEFEH	GKSRIALTNS	VNEALLNPSR	VYTFSSDYV	KKVKNKATEAA 600
601	MFLGWVEQLV	YDFTDETSEV	STTDKIADIT	IIIPYIGPAL	NIGNMLYKDD	FVGALIFSGA 660
661	VILLEFIPEI	AIPVLGTFAL	VSYIANKVLT	VQTIDNALS	RNEKWDEVYK	YIVTNWLAKV 720
721	NTQIDILIRK	MKEALENQAE	ATKAIINYQY	NQYTEEEKNN	INFNIDDLSS	KLNESINKAM 780
781	ININKFLNQC	SVSYLMNSMI	PYGVKRLEDF	DASLKDALLK	YIYDNRGTLI	GQVDRDKDKV 840
841	NNTLSTDIPF	QLSKYVDNQR	LLSTFTEYIK	NIINTSILNL	RYESNHLIDL	SRYASKINIG 900
901	SKVNFDPIDK	NQIQLFNLES	SKIEVILKNA	IVYNSMYENF	STSFWIRIPK	YFNSISLNNE 960
961	YTIINCMENN	SGWKVSLNYG	EIIWTLQDTQ	EIKQRVVFKY	SQMINISDYI	NRWIFVTITN 1020
1021	NRLNNSKIYI	NGRLIDQKPI	SNLGNIHASN	NIMFKLDGCR	DTHRYIWIYK	FNLFDKELNE 1080
1081	KEIKDLYDNQ	SNSGILKDFW	GDYLYQDKPY	YMLNLYDPNK	YVDVNNVGIR	GYMYLKGPGRG 1140
1141	SVMTTNIYLN	SSLYRGTKFI	IKKYASGNKD	NIVRNNDRVY	INVVVKNKEY	RLATNASQAG 1200
1201	VEKILSALEI	PDVGNLSQVV	VMKSKNDQGI	TNKCKMNLQD	NNGNDIGFIG	FHQFNNIACL 1260
1261	VASNWYNRQI	ERSSRTLGC	WEFIPVDDGW	GERPL		

In three-letter code:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	
1	Pro	Phe	Val	Asn	Lys	Gln	Phe	Asn	Tyr	Lys	Asp	Pro	Val	Asn	Gly	15
16	Val	Asp	Ile	Ala	Tyr	Ile	Lys	Ile	Pro	Asn	Val	Gly	Gln	Met	Gln	30
31	Pro	Val	Lys	Ala	Phe	Lys	Ile	His	Asn	Lys	Ile	Trp	Val	Ile	Pro	45
46	Glu	Arg	Asp	Thr	Phe	Thr	Asn	Pro	Glu	Glu	Gly	Asp	Leu	Asn	Pro	60
61	Pro	Pro	Glu	Ala	Lys	Gln	Val	Pro	Val	Ser	Tyr	Tyr	Asp	Ser	Thr	75
76	Tyr	Leu	Ser	Thr	Asp	Asn	Glu	Lys	Asp	Asn	Tyr	Leu	Lys	Gly	Val	90
91	Thr	Lys	Leu	Phe	Glu	Arg	Ile	Tyr	Ser	Thr	Asp	Leu	Gly	Arg	Met	105
106	Leu	Leu	Thr	Ser	Ile	Val	Arg	Gly	Ile	Pro	Phe	Trp	Gly	Gly	Ser	120
121	Thr	Ile	Asp	Thr	Glu	Leu	Lys	Val	Ile	Asp	Thr	Asn	Cys	Ile	Asn	135
136	Val	Ile	Gln	Pro	Asp	Gly	Ser	Tyr	Arg	Ser	Glu	Glu	Leu	Asn	Leu	150
151	Val	Ile	Ile	Gly	Pro	Ser	Ala	Asp	Ile	Ile	Gln	Phe	Glu	Cys	Lys	165
166	Ser	Phe	Gly	His	Glu	Val	Leu	Asn	Leu	Thr	Arg	Asn	Gly	Tyr	Gly	180
181	Ser	Thr	Gln	Tyr	Ile	Arg	Phe	Ser	Pro	Asp	Phe	Thr	Phe	Gly	Phe	195
196	Glu	Glu	Ser	Leu	Glu	Val	Asp	Thr	Asn	Pro	Leu	Leu	Gly	Ala	Gly	210



211 Lys Phe Ala Thr Asp Pro Ala Val Thr Leu Ala His Glu Leu Ile 225  
 226 His Ala Gly His Arg Leu Tyr Gly Ile Ala Ile Asn Pro Asn Arg 240  
 241 Val Phe Lys Val Asn Thr Asn Ala Tyr Tyr Glu Met Ser Gly Leu 255  
 256 Glu Val Ser Phe Glu Glu Leu Arg Thr Phe Gly Gly His Asp Ala 270  
 271 Lys Phe Ile Asp Ser Leu Gln Glu Asn Glu Phe Arg Leu Tyr Tyr 285  
 286 Tyr Asn Lys Phe Lys Asp Ile Ala Ser Thr Leu Asn Lys Ala Lys 300  
 301 Ser Ile Val Gly Thr Thr Ala Ser Leu Gln Tyr Met Lys Asn Val 315  
 316 Phe Lys Glu Lys Tyr Leu Leu Ser Glu Asp Thr Ser Gly Lys Phe 330  
 331 Ser Val Asp Lys Leu Lys Phe Asp Lys Leu Tyr Lys Met Leu Thr 345  
 346 Glu Ile Tyr Thr Glu Asp Asn Phe Val Lys Phe Phe Lys Val Leu 360  
 361 Asn Arg Lys Thr Tyr Leu Asn Phe Asp Lys Ala Val Phe Lys Ile 375  
 376 Asn Ile Val Pro Lys Val Asn Tyr Thr Ile Tyr Asp Gly Phe Asn 390  
 391 Leu Arg Asn Thr Asn Leu Ala Ala Asn Phe Asn Gly Gln Asn Thr 405  
 406 Glu Ile Asn Asn Met Asn Phe Thr Lys Leu Lys Asn Phe Thr Gly 420  
 421 Leu Phe Glu Phe Tyr Lys Leu Leu Cys Val Arg Gly Ile Ile Thr 435  
 436 Ser Lys Thr Lys Ser Leu Asp Lys Gly Tyr Asn Lys Ala Leu Asn 450  
 451 Asp Leu Cys Ile Lys Val Asn Asn Trp Asp Leu Phe Phe Ser Pro 465  
 466 Ser Glu Asp Asn Phe Thr Asn Asp Leu Asn Lys Gly Glu Glu Ile 480  
 481 Thr Ser Asp Thr Asn Ile Glu Ala Ala Glu Glu Asn Ile Ser Leu 495  
 496 Asp Leu Ile Gln Gln Tyr Tyr Leu Thr Phe Asn Phe Asp Asn Glu 510  
 511 Pro Glu Asn Ile Ser Ile Glu Asn Leu Ser Ser Asp Ile Ile Gly 525  
 526 Gln Leu Glu Leu Met Pro Asn Ile Glu Arg Phe Pro Asn Gly Lys 540  
 541 Lys Tyr Glu Leu Asp Lys Tyr Thr Met Phe His Tyr Leu Arg Ala 555  
 556 Gln Glu Phe Glu His Gly Lys Ser Arg Ile Ala Leu Thr Asn Ser 570  
 571 Val Asn Glu Ala Leu Leu Asn Pro Ser Arg Val Tyr Thr Phe Phe 585  
 586 Ser Ser Asp Tyr Val Lys Lys Val Asn Lys Ala Thr Glu Ala Ala 600  
 601 Met Phe Leu Gly Trp Val Glu Gln Leu Val Tyr Asp Phe Thr Asp 615  
 616 Glu Thr Ser Glu Val Ser Thr Thr Asp Lys Ile Ala Asp Ile Thr 630  
 631 Ile Ile Ile Pro Tyr Ile Gly Pro Ala Leu Asn Ile Gly Asn Met 645  
 646 Leu Tyr Lys Asp Asp Phe Val Gly Ala Leu Ile Phe Ser Gly Ala 660  
 661 Val Ile Leu Leu Glu Phe Ile Pro Glu Ile Ala Ile Pro Val Leu 675  
 676 Gly Thr Phe Ala Leu Val Ser Tyr Ile Ala Asn Lys Val Leu Thr 690  
 691 Val Gln Thr Ile Asp Asn Ala Leu Ser Lys Arg Asn Glu Lys Trp 705  
 706 Asp Glu Val Tyr Lys Tyr Ile Val Thr Asn Trp Leu Ala Lys Val 720  
 721 Asn Thr Gln Ile Asp Leu Ile Arg Lys Lys Met Lys Glu Ala Leu 735  
 736 Glu Asn Gln Ala Glu Ala Thr Lys Ala Ile Ile Asn Tyr Gln Tyr 750  
 751 Asn Gln Tyr Thr Glu Glu Glu Lys Asn Asn Ile Asn Phe Asn Ile 765  
 766 Asp Asp Leu Ser Ser Lys Leu Asn Glu Ser Ile Asn Lys Ala Met 780  
 781 Ile Asn Ile Asn Lys Phe Leu Asn Gln Cys Ser Val Ser Tyr Leu 795  
 796 Met Asn Ser Met Ile Pro Tyr Gly Val Lys Arg Leu Glu Asp Phe 810  
 811 Asp Ala Ser Leu Lys Asp Ala Leu Leu Lys Tyr Ile Tyr Asp Asn 825  
 826 Arg Gly Thr Leu Ile Gly Gln Val Asp Arg Leu Lys Asp Lys Val 840  
 841 Asn Asn Thr Leu Ser Thr Asp Ile Pro Phe Gln Leu Ser Lys Tyr 855  
 856 Val Asp Asn Gln Arg Leu Leu Ser Thr Phe Thr Glu Tyr Ile Lys 870  
 871 Asn Ile Ile Asn Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn 885  
 886 His Leu Ile Asp Leu Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly 900  
 901 Ser Lys Val Asn Phe Asp Pro Ile Asp Lys Asn Gln Ile Gln Leu 915  
 916 Phe Asn Leu Glu Ser Ser Lys Ile Glu Val Ile Leu Lys Asn Ala 930  
 931 Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser Thr Ser Phe Trp 945  
 946 Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu Asn Asn Glu 960  
 961 Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp Lys Val 975  
 976 Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr Gln 990  
 991 Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn 1005  
 1006 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn 1020  
 1021 Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile 1035  
 1036 Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn 1050  
 1051 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr 1065  
 1066 Ile Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu 1080  
 1081 Lys Glu Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile 1095  
 1096 Leu Lys Asp Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr 1110

1111 Tyr Met Leu Asn Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn 1125  
1126 Asn Val Gly Ile Arg Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly 1140  
1141 Ser Val Met Thr Thr Asn Ile Tyr Leu Asn Ser Ser Leu Tyr Arg 1155  
1156 Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala Ser Gly Asn Lys Asp 1170  
1171 Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile Asn Val Val Val 1185  
1186 Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser Gln Ala Gly 1200  
1201 Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val Gly Asn 1215  
1216 Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly Ile 1230  
1231 Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp 1245  
1246 Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu 1260  
1261 Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg 1275  
1276 Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp 1290  
1291 Gly Glu Arg Pro Leu

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